SEQUENCE LISTING

(1) GENERAL INFORMATION:

    (i) APPLICANT:
        (A) NAME: Koninklijke Universiteit Nijmegen,
               Afdeling tumorimmunologie
        (B) STREET: Philips van Leydenlaan 25
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    (v) COMPUTER READABLE FORM:
        (A) MEDIUM TYPE: Floppy disk
        (B) COMPUTER: IBM PC compatible
        (C) OPERATING SYSTEM: PC-DOS/MS-DOS
        (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

    (ii) TITLE OF INVENTION: COMPOSITION AND METHOD FOR MODULATING
DENDRITIC CELL-T CELL INTERACTION

    (iii) NUMBER OF SEQUENCES: 2

(2) INFORMATION FOR SEQ ID NO:1:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 1215 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA

    (iii) HYPOTHETICAL: NO

    (iv) ANTI-SENSE: NO

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATGAGTGACT CCAAGGAACC AAGACTGCAG CAGCTGGGCC TCCTGGAGGA GGAACAGCTG   60

AGAGGCCTTG GATTCCGACA GACTCGAGGA TACAAGAGCT TAGCAGGGTG TCTTGGCCAT   120

GGTCCCCTGG TGCTGCAACT CCTCTCCTTC ACGCTCTTGG CTGGGCTCCT TGTCCAAGTG   180

TCCAAGGTCC CCAGCTCCAT AAGTCAGGAA CAATCCAGGC AAGACGCGAT CTACCAGAAC   240

CTGACCCAGC TTAAAGCTGC AGTGGGTGAG CTCTCAGAGA AATCCAAGCT GCAGGAGATC   300

TACCAGGAGC TGACCCAGCT GAAGGCTGCA GTGGGTGAGC TTCCAGAGAA ATCTAAGCTG   360

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CAGGAGATCT ACCAGGAGCT GACCCGGCTG AAGGCTGCAG TGGGTGAGCT TCCAGAGAAA    420

TCTAAGCTGC AGGAGATCTA CCAGGAGCTG ACCTGGCTGA AGGCTGCAGT GGGTGAGCTT    480

CCAGAGAAAT CTAAGATGCA GGAGATCTAC CAGGAGCTGA CTCGGCTGAA GGCTGCAGTG    540

GGTGAGCTTC CAGAGAAATC TAAGCAGCAG GAGATCTACC AGGAGCTGAC CCGGCTGAAG    600

GCTGCAGTGG GTGAGCTTCC AGAGAAATCT AAGCAGCAGG AGATCTACCA GGAGCTGACC    660

CGGCTGAAGG CTGCAGTGGG TGAGCTTCCA GAGAAATCTA AGCAGCAGGA GATCTACCAG    720

GAGCTGACCC AGCTGAAGGC TGCAGTGGAA CGCCTGTGCC ACCCCTGTCC CTGGGAATGG    780

ACATTCTTCC AAGGAAACTG TTACTTCATG TCTAACTCCC AGCGGAACTG GCACGACTCC    840

ATCACCGCCT GCAAAGAAGT GGGGGCCCAG CTCGTCGTAA TCAAAAGTGC TGAGGAGCAG    900

AACTTCCTAC AGCTGCAGTC TTCCAGAAGT AACCGCTTCA CCTGGATGGG ACTTTCAGAT    960

CTAAATCAGG AAGGCACGTG GCAATGGGTG GACGGCTCAC CTCTGTTGCC CAGCTTCAAG    1020

CAGTATTGGA ACAGAGGAGA GCCCAACAAC GTTGGGGAGG AAGACTGCGC GGAATTTAGT    1080

GGCAATGGCT GGAACGACGA CAAATGTAAT CTTGCCAAAT TCTGGATCTG CAAAAAGTCC    1140

GCAGCCTCCT GCTCCAGGGA TGAAGAACAG TTTCTTTCTC CAGCCCCTGC CACCCCAAAC    1200

CCCCCTCCTG CGTAG                                                    1215
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2) INFORMATION FOR SEQ ID NO:2:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 415 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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Met Ser Asp Ser Lys Glu Pro Arg Leu Gln Gln Leu Gly Leu Leu
 1               5                  10                  15

Glu Glu Glu Gln Leu Arg Gly Leu Gly Phe Arg Gln Thr Arg Gly
                20                  25                  30

Tyr Lys Ser Leu Ala Gly Cys Leu Gly His Gly Pro Leu Val Leu
                35                  40                  45

Gln Leu Leu Ser Phe Thr Leu Leu Ala Gly Leu Leu Val Gln Val
                50                  55                  60
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Ser Lys Val Pro Ser Ser Ile Ser Gln Glu Gln Ser Arg Gln Asp
            65   70   75

5

Ala Ile Tyr Gln Asn Leu Thr Gln Leu Lys Ala Ala Val Gly Glu
            80   85   90

Leu Ser Glu Lys Ser Lys Leu Gln Glu Ile Tyr Gln Glu Leu Thr
            95   100   105

10

Gln Leu Lys Ala Ala Val Gly Glu Leu Pro Glu Lys Ser Lys Leu
            110   115   120

Gln Glu Ile Tyr Gln Glu Leu Thr Arg Leu Lys Ala Ala Val Gly
            125   130   135

15

Glu Leu Pro Glu Lys Ser Lys Leu Gln Glu Ile Tyr Gln Glu Leu
            140   145   150

Thr Trp Leu Lys Ala Ala Val Gly Glu Leu Pro Glu Lys Ser Lys
            155   160   165

20

Met Gln Glu Ile Tyr Gln Glu Leu Thr Arg Leu Lys Ala Ala Val
            170   175   180

25

Gly Glu Leu Pro Glu Lys Ser Lys Gln Gln Glu Ile Tyr Gln Glu
            185   190   195

Leu Thr Arg Leu Lys Ala Ala Val Gly Glu Leu Pro Glu Lys Ser
            200   205   210

30

Lys Gln Gln Glu Ile Tyr Gln Glu Leu Thr Arg Leu Lys Ala Ala
            215   220   225

Val Gly Glu Leu Pro Glu Lys Ser Lys Gln Gln Glu Ile Tyr Gln
            230   235   240

35

Glu Leu Thr Gln Leu Lys Ala Ala Val Glu Arg Leu Cys His Pro
            245   250   255

40

Cys Pro Trp Glu Trp Thr Phe Phe Gln Gly Asn Cys Tyr Phe Met
            260   265   270

Ser Asn Ser Gln Arg Asn Trp His Asp Ser Ile Thr Ala Cys Lys
            275   280   285

45

Glu Val Gly Ala Gln Leu Val Val Ile Lys Ser Ala Glu Glu Gln
            290   295   300

50

Asn Phe Leu Gln Leu Gln Ser Ser Arg Ser Asn Arg Phe Thr Trp
            305   310   315

Met Gly Leu Ser Asp Leu Asn Gln Glu Gly Thr Trp Gln Trp Val
            320   325   330

55

Asp Gly Ser Pro Leu Leu Pro Ser Phe Lys Gln Tyr Trp Asn Arg
        335   340   345

5   Gly Glu Pro Asn Asn Val Gly Glu Glu Asp Cys Ala Glu Phe Ser
        350   355   360

Gly Asn Gly Trp Asn Asp Asp Lys Cys Asn Leu Ala Lys Phe Trp
        365   370   375

10   Ile Cys Lys Lys Ser Ala Ala Ser Cys Ser Arg Asp Glu Glu Gln
        380   385   390

Phe Leu Ser Pro Ala Pro Ala Thr Pro Asn Pro Pro Pro Ala   *
        395   400   404

15